

コムギ品種のイネ科植物うどんこ病菌(*Erysiphe graminis* DC.) の分化型に対する抵抗性の遺伝学的解析

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著者名	奥,尚 山下,修一 土居,養二 日浦,運治
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Genetic Analysis of Resistance of Wheat Cultivars to Races and Some Formae Speciales of *Erysiphe graminis* DC.

Takashi OKU*, Shuichi YAMASHITA*, Yoji DOI* and Unji HIURA**

Abstract

Genes for powdery mildew resistance in wheat cultivars were characterized by their responses to *Erysiphe graminis* f. sp. *tritici* culture t4 and some synthetic hybrid cultures derived from crossing between *E. graminis* f. sp. *tritici* culture t2 and f. sp. *agropyri* culture A1, and between culture t2 and f. sp. *secalis* culture S1. Hybrid cultures were less virulent to wheat cultivars of different genetic backgrounds comparing with the parent culture t2, and several wheat cultivars which were inherently susceptible to t2 and t4 were found to be resistant to hybrid cultures. Inoculation tests with F₂ progenies indicated that cultivars exhibited resistance to hybrid cultures, such as Little Club, Mayo 64, Sinvalucho and Hard Federation, had one recessive or one dominant gene for resistance different from *Pm1*, *Pm2*, *Pm3a* and *Pm4a*. However, one near-isogenic line of Chancellor origin, Axminster × Cc⁸, which is known to possess one dominant gene for resistance (*Pm1*), was resistant to t4 as well as to one of the hybrid cultures. The facts that hybrid cultures between formae speciales caused intermediate reactions of parent cultures in wheat cultivars and that wheat genes for resistance to hybrid cultures could not be essentially distinguished from genes for races of *E. graminis* f. sp. *tritici*, indicated that difference of pathogenicity in f. sp. *tritici*, f. sp. *agropyri* and f. sp. *secalis* of *E. graminis* to wheat cultivars is due to the degree of accumulation of virulent genes to wheat.

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Key words : genetic analysis, wheat resistance, formae speciales, *Erysiphe graminis*.

Introduction

Seven formae speciales (f. sp.) are known in *Erysiphe graminis* DC., the causal fungus of cereal powdery mildews ; namely f. sp. *agropyri*, *avenae*, *bromi*, *hordei*, *poae*, *secalis* and *tritici*. In Japan, f. sp. *avenae* has not found, but the existence of f. sp. *dactylidis* was reported recently¹⁹⁾. In spite of these clear specialization, very little is known about the genetic and physiological basis of formae speciales. Since ascospores are, like conidia, pathogenic only to the host genus from which they had been isolated^{16, 17, 19, 20, 22)}, it has been thought that the hybridizations in *E. graminis* occur within the same formae speciales. However, heterothallism was demonstrated in some combinations of formae speciales by artificial cross⁶⁾ and subsequent confirmation of the survival of hybrid progenies⁷⁾. Genetics of specific pathogenicity in these formae speciales were studied by

* Faculty of Agriculture, University of Tokyo, Bunkyo-Ku, Tokyo 113, Japan 東京大学農学部

** Institute for Agricultural and Biological Science, Okayama University, Kurashiki-City, Okayama 710, Japan 岡山大学農業生物研究所

using such progenies^{5,8-13,18}).

In this paper, we report the results of experiment aimed at clarifying the difference of resistant genes in wheat cultivars on the basis of responses to f. sp. *tritici* and to some synthetic hybrids between formae speciales of *E. graminis*.

Materials and Methods

Powdery mildew fungi. Cultures of *Erysiphe graminis* used in this study were monoconidial ones; t4 and t2 of f. sp. *tritici* from wheat (*Triticum aestivum* (L.) Thell.) A1 of f. sp. *agropyri* from wheatgrass (*Agropyron tsukushiense* var. *transiens* Ohwi), S1 of f. sp. *secalis* from rye (*Secale cereale* L.), hybrids AT-N23 and AT-C8 from the cross between t2 and A1, and hybrid ST-N14 from the cross between t2 and S1. The hybridization procedure between formae speciales was described previously^{6,7}. AT-N23 and ST-N14 were isolated on wheat cv. Norin 4. AT-C8 was isolated on wheat cv. Chancellor. Cultures t4, t2, AT-N23, AT-C8 and ST-N14 were maintained on leaves of wheat cv. Norin 4, A1 on wheatgrass strain Mishima and S1 on rye cv. Petkus, respectively. The host plants were grown on clay in cotton-plugged test tubes of 30×300 mm under the constant illumination of 3,000 lux fluorescent lamp at 20 C. Each culture was inoculated to each host plants at 1-2 leaf stage with soft hair pencil. Three days after inoculation, plants in test tubes were stocked at 5 C under constant illumination of 2,000 lux until use.

Wheat cultivars. Wheat cultivars used were obtained from the Second Division of Plant Pathology, Institute for Agricultural and Biological Science, Okayama University. Each of ($\times$ Cc⁸) was near-isogenic lines of wheat cv. Chancellor possessing one gene for resistance to *E. graminis* f. sp. *tritici*^{1,15}).

Inoculation and reaction evaluation. Inocula were obtained from leaves of 1-2 leaf stage seedlings of appropriate cultivars which had been inoculated and incubated for about 1 week in a greenhouse at 20 C. To prevent contamination, cultures were separated from each other.

Test plants were inoculated at 1-2 leaf stage with conidia of each culture in the inoculation room. By shaking the colonized plants above the test plants, conidia were sprinkled over the plants. After 3-day incubation in the room, the inoculated plants were transferred into greenhouse. Each leaf was cut off, and put into 20×300 mm test tube containing 3 ml water. They were kept in greenhouse for another 4-6 days, and their reactions were examined classifying them into five (0-4) infection types³⁹.

Genetic analysis. Highly resistant wheat cultivars with infection type 0 or 0-1 were used as a resistant gene source. These resistant cultivars were crossed with susceptible cultivars or other resistant cultivars, and F₂ progenies were subjected to inoculation test with each culture of *E. graminis*. Genetic analysis was made on the basis of segregation ratio of resistant and susceptible F₂ progenies. The resistance or susceptibility of F₂ progenies was determined by comparing the observed infection types with that of each parent wheat cultivar which had been inoculated simultaneously. The segregation ratio was subjected to Chi-square test.

Results

Reaction of wheat cultivars to each forma specialis and their hybrids

Results of inoculation experiments with culture t4 and parent cultures t2, A1 and S1 used for hybridization on wheat cultivars, wheatgrass and rye were summarized in Table 1. Cultures t2 and t4 isolated from wheat were mainly pathogenic to wheat cul-

Table 1. Infection type on wheat cultivars, wheatgrass and rye by parent culture of *Erysiphe graminis*

Cultivar	Culture of <i>E. graminis</i>			
	t 2 ^{a)}	t 4 ^{a)}	A 1 ^{b)}	S 1 ^{c)}
Norin 4	4 ^{d)}	4	0	0
Sinvalucho	4	4	0	0
Little Club	4	4	0	0
Hard Federation	4	4	0	0
Ramona 50	4	0-1	0	0
Chancellor	4	4	0	0
Axminster × Cc ^{8 e)} (Pm 1)	4	0	0	0
Ulka × Cc ^{8 e)} (Pm 2)	0	0	0	0
Asosan × Cc ^{8 e)} (Pm3a)	1-2	0	0	0
Khapli × Cc ^{8 e)} (Pm4a)	0	0	0	0
Agt. strain Mishima ^{f)}	0	0	4	0
Petkus-rye ^{g)}	0	0	0	3-4

a) Isolate from wheat (*Triticum aestivum* (L.) Thell.).

b) Isolate from wheatgrass (*Agropyron tsukushiense* var. *transiens* Ohwi).

c) Isolate from rye (*Secale cereale* L.).

d) 4 : Highly susceptible, 0 : highly resistant (after Finkner *et al.*³⁾).

e) Near-isogenic line of Chancellor wheat possessing one gene for resistance to *E. graminis* f. sp. *tritici*.

f) Wheatgrass.

g) Rye.

tivars, and cultures A1 and S1 were pathogenic to respective host plant, wheatgrass and rye. Therefore, isolates t2 and t4 fell into the category of f. sp. *tritici*, A1 into f. sp. *agropyri* and S1 into f. sp. *secalis*.

Table 2 shows the reaction of various wheat cultivars to hybrid cultures obtained from crossing between f. sp. *tritici* and f. sp. *agropyri* or f. sp. *secalis*. All the hybrid cultures, AT-N23, AT-C8 and ST-N14, were less pathogenic to wheat cultivars than their parent t2. It should be mentioned here that wheat cultivars in which no resistant gene to powdery mildew had been identified, were resistant to hybrid cultures.

Gene for resistance to culture t4

Segregation of resistant and susceptible progenies in F₂ generation from crosses of wheat cultivars against culture t4 is shown in Table 3.

Segregation ratios in crosses, susceptible × resistant and resistant × resistant, indicated that each of Axminster × Cc⁸, Ulka × Cc⁸, Asosan × Cc⁸ and Khapli × Cc⁸ had one dominant gene for resistance, and Ramona 50 had one recessive resistant gene.

Table 2. Infection type on wheat cultivars of synthetic hybrids between formae speciales of *Erysiphe graminis*

Cultivar	Culture of <i>E. graminis</i>		
	AT-N23 ^{a)}	AT-C8 ^{a)}	ST-N14 ^{b)}
Norin 4	3	3-4	3
Sinvalucho	3	0-1	3
Little Club	0-1	0-1	0
Hard Federation	0-1	3-4	1-2
Ramona 50	0	3-4	1
Mayo 64	3	0-1	0-1
Axminster $\times$ Cc ^{8 c)} (Pm1)	2	0-1	1-2
Ulka $\times$ Cc ^{8 c)} (Pm2)	0	0-1	0
Asosan $\times$ Cc ^{8 c)} (Pm3a)	0	2	1-2
Khapli $\times$ Cc ^{8 c)} (Pm4a)	0	0	0

a) Hybrid culture from the cross of culture t2 of *E. graminis* f. sp. *tritici* and culture Al of *E. graminis* f. sp. *agropyri*.

b) Hybrid culture from the cross of culture t2 and culture S1 of *E. graminis* f. sp. *secalis*.

c) See footnote of Table 1.

Table 3. Segregation of resistant and susceptible progenies at F₂ generation from crosses of wheat cultivars assessed by inoculating with a culture t4 of *Erysiphe graminis* f. sp. *tritici*

Cross		No. of F ₂ plants		P for (ratio)
		Resistant	Susceptible	
S	$\times$ R			
Norin 4	$\times$ (Axminster $\times$ Cc ⁸)	172	44	0.1-0.2 (3 : 1)
Norin 4	$\times$ (Ulka $\times$ Cc ⁸)	243	75	0.5-0.7 (3 : 1)
Norin 4	$\times$ (Asosan $\times$ Cc ⁸)	251	90	0.5-0.7 (3 : 1)
Norin 4	$\times$ (Khapli $\times$ Cc ⁸)	245	102	0.05-0.1 (3 : 1)
Sinvalucho	$\times$ Ramona 50	36	90	0.5-0.7 (1 : 3)
R	$\times$ R			
Ramona 50	$\times$ (Ulka $\times$ Cc ⁸)	292	37	small (13 : 3)
Ramona 50	$\times$ (Asosan $\times$ Cc ⁸)	271	12	small (13 : 3)
Ramona 50	$\times$ (Khapli $\times$ Cc ⁸)	236	46	0.2-0.3 (13 : 3)

Data obtained from the cross between resistant cv. Ramona 50 $\times$ (Khapli $\times$ Cc⁸) fit to the segregation ratio 13 : 3. In the cross Ramona 50 $\times$ (Ulka $\times$ Cc⁸), (Asosan $\times$ Cc⁸), segregation ratio did not fit to 13 : 3 for R : S, but susceptible progenies were segregated. Thus the locus of resistant gene of Ramona 50 seemed to be different from those of Ulka $\times$ Cc⁸, Asosan $\times$ Cc⁸ and Khapli $\times$ Cc⁸. Cross Ramona 50 $\times$ (Axminster $\times$ Cc⁸) was not tested.

Gene for resistance to culture AT-N23

Segregation of resistant and susceptible progenies against AT-N23 in F₂ generation from crosses of wheat cultivars is shown in Table 4. The number of progenies which fit to the ratio 3 : 1 for R : S, as observed in Hard Federation, Ramona 50, (Ulka $\times$

Table 4. Segregation of resistant and susceptible progenies at F_2 generation from crosses of wheat cultivars as evaluated by the responses to a hybrid culture AT-N23 of *Erysiphe graminis*

Cross		No. of F_2 plants		P for (ratio)
		Resistant	Susceptible	
S	× R			
Norin 4	× Hard Federation	195	82	0.05—0.1 (3 : 1)
Norin 4	× Ramona 50	210	76	0.5—0.7 (3 : 1)
Norin 4	× Little Club	72	216	>0.95 (1 : 3)
Norin 4	× (Ulka × Cc ⁸)	183	70	0.7—0.8 (3 : 1)
Norin 4	× (Asosan × Cc ⁸)	251	90	0.5—0.7 (3 : 1)
Norin 4	× (Khapli × Cc ⁸)	206	68	>0.95 (3 : 1)
R	× R			
Ramona 50	× Little Club	391	0	
Ramona 50	× Hard Federation	206	0	
Ramona 50	× (Ulka × Cc ⁸)	230	19	0.3—0.5 (15 : 1)
Ramona 50	× (Asosan × Cc ⁸)	261	22	0.2—0.3 (15 : 1)
Ramona 50	× (Khapli × Cc ⁸)	225	20	0.2—0.3 (15 : 1)
Hard Federation	× (Ulka × Cc ⁸)	144	11	0.2—0.3 (15 : 1)
Little Club	× (Ulka × Cc ⁸)	213	24	small (13 : 3)
Little Club	× (Khapli × Cc ⁸)	214	17	small (13 : 3)

Cc⁸), (Asosan × Cc⁸) and (Khapli × Cc⁸) × Norin 4, indicated that each resistant cultivar involves one dominant gene for resistance. Segregation ratio in Norin 4 × Little Club fit to the ratio of 1 : 3, indicated that cv. Little Club involves one recessive gene for resistance against AT-N23. Data derived from crosses between resistant cultivars indicated that resistant genes in Little Club, Hard Federation and Ramona 50 are linked, but different from genes known as *Pm2*, *Pm3a* and *Pm4a*.

Gene for resistance to culture AT-C8

To analyze the resistant genes of Little Club, Mayo 64, Sinvalucho, Axminster × Cc⁸ and Ulka × Cc⁸ against hybrid culture AT-C8, these cultivars were crossed with a susceptible cultivar, Norin 4, and the segregation ratio for R : S in F_2 progenies against AT-C8 was examined (Table 5). The segregation ratio for R : S fit to 3 : 1 in crosses between Norin 4 and Mayo 64, Sinvalucho, (Axminster × Cc⁸) and (Ulka × Cc⁸). These results show that each of these resistant cultivars have one dominant gene for resistance. In Norin 4 × Little Club, the segregation ratio for R : S was 1 : 3, hence Little Club may have one recessive gene for resistance. Further segregation ratio of F_2 progenies of Mayo 64 × (Axminster × Cc⁸), (Ulka × Cc⁸), Little Club and Sinvalucho was examined to compare the locus of resistant genes. In Mayo 64 × (Axminster × Cc⁸), (Ulka × Cc⁸), the segregation ratio for R : S fit to 15 : 1 indicating that the resistant genes in these cultivars are inherited independently. However, segregation of susceptible progenies was extremely low in crosses, Mayo 64 × Little Club and Mayo 64 × Sinvalucho, suggesting that the resistant genes to AT-C8 may probably be linked closely.

Gene for resistance to culture ST-N14

Segregation of resistant and susceptible progenies in F_2 generation of several crosses

Table 5. Segregation of resistant and susceptible progenies at F_2 generation from crosses of wheat cultivars as evaluated by the responses to a hybrid culture AT-C8 of *Erysiphe graminis*

Cross			No. of F_2 plants		P for (ratio)
			Resistant	Susceptible	
S	×	R			
Norin 4	×	Little Club	38	150	0.1–0.2 (1 : 3)
Norin 4	×	Mayo 64	136	56	0.3–0.5 (3 : 1)
Norin 4	×	Sinvalucho	114	51	0.05–0.1 (3 : 1)
Norin 4	×	(Axminster × Cc ⁸)	48	20	0.3–0.5 (3 : 1)
Norin 4	×	(Ulka × Cc ⁸)	85	28	>0.95 (3 : 1)
R	×	R			
Mayo 64	×	Little Club	251	1	
Mayo 64	×	Sinvalucho	101	2	
Mayo 64	×	(Axminster × Cc ⁸)	173	11	0.9–0.95 (15 : 1)
Mayo 64	×	(Ulka × Cc ⁸)	160	7	0.2–0.3 (15 : 1)

Table 6. Segregation of resistant and susceptible progenies at F_2 generation from crosses of wheat cultivars as evaluated by the responses to a hybrid culture ST-N14 of *Erysiphe graminis*

Cross			No. of F_2 plants		P for (ratio)
			Resistant	Susceptible	
S	×	R			
Norin 4	×	Little Club	62	198	0.5–0.7 (1 : 3)
Sinvalucho	×	Mayo 64	68	254	0.1–0.2 (1 : 3)
Norin 4	×	(Ulka × Cc ⁸)	181	72	0.2–0.3 (3 : 1)
Norin 4	×	(Khapli × Cc ⁸)	206	68	>0.95 (3 : 1)
R	×	R			
Little Club	×	Mayo 64	440	0	
Little Club	×	(Ulka × Cc ⁸)	196	41	0.5–0.7 (13 : 3)
Little Club	×	(Khapli × Cc ⁸)	201	31	0.02–0.05 (13 : 3)
Mayo 64	×	(Ulka × Cc ⁸)	197	33	0.05–0.1 (13 : 3)
Mayo 64	×	(Khapli × Cc ⁸)	181	60	0.01–0.02 (13 : 3)

against hybrid culture ST-N14 is shown in Table 6.

Cultivars Little Club and Mayo 64 are susceptible to t2, a parent culture of ST-N14, and no resistant gene has so far been reported in these cultivars. Norin 4 and Sinvalucho were susceptible to ST-N14. F_2 progenies from the crosses Little Club × Norin 4 and Sinvalucho × Mayo 64 segregated into 1 : 3 for R : S. These data indicated that both Little Club and Mayo 64 have one recessive gene for resistance against ST-N14. The other two F_2 progenies from Norin 4 × (Ulka × Cc⁸) and Norin 4 × (Khapli × Cc⁸) segregated into 3 : 1 for R : S, indicating that Ulka × Cc⁸ and Khapli × Cc⁸ have one dominant gene for resistance.

To compare the loci of these recessive and dominant genes, F_2 progenies from Little Club × (Ulka × Cc⁸), Little Club × (Khapli × Cc⁸), Mayo 64 × (Ulka × Cc⁸) and Mayo

64 $\times$ (Khapli $\times$ Cc⁸) were subjected to inoculation with ST-N14 (Table 6). The segregation ratio for R : S was 13 : 3 in progenies of Little Club $\times$ (Ulka $\times$ Cc⁸) and Mayo 64 $\times$ (Ulka $\times$ Cc⁸) indicating that these resistant genes are inherited independently. From the crosses Little Club $\times$ (Khapli $\times$ Cc⁸) and Mayo 64 $\times$ (Khapli $\times$ Cc⁸), segregation ratio for R : S did not fit to 13 : 3, but susceptible progenies were segregated. This fact suggests that the locus of resistant gene in Little Club and Khapli $\times$ Cc⁸, in Mayo 64 and Khapli $\times$ Cc⁸ may be different. The data of F₂ analysis from the cross the cross Mayo 64 $\times$ Little Club against ST-N14 suggests that the resistant gene in both cultivars is on the same locus or tightly linked. Namely, in this cross, no susceptible F₂ was segregated.

Discussion

Erysiphe graminis f. sp. *tritici* cultures t2 and t4, f. sp. *agropyri* culture A1 and f. sp. *secalis* culture S1 are pathogenic strictly on wheat, wheatgrass and rye, respectively, and do not invade plants other than their own host. A wheat fungus, t2 could be hybridized with A1 and S1 freely on wheatgrass or rye, in spite of its inability to infect the both plant species. Both hybrid cultures AT-N23 and AT-C8 derived from A1 $\times$ t2, and ST-N14 from S1 $\times$ t2 could invade wheat cv. Norin 4, but showed different infectivity from the parent culture t2, on several wheat cultivars. The reduction of pathogenicity in hybrid cultures to wheat cultivars as compared with the parent culture t2 could be explained as follows : The wheat fungus accumulated many genes for virulence to wheat, and some of which were substituted by avirulent genes of A1 or S1 by hybridization. On the contrary, the other parent culture A1 or S1 might have accumulated many virulent genes to respective host plant and corresponding avirulent genes against wheat, as Johnson pointed out¹⁴⁾. Therefore, these fungal cultures most likely belong to the same species, and probably have same genetic loci for pathogenicity.

Recent works on the pathogenicity of hybrids between formae speciales of *Puccinia graminis*^{2,23)} indicated that susceptible plants to their own forma specialis were having genes for resistance to other formae speciales, and some known resistant genes did not function to hybrid cultures.

Hiura *et al.*¹³⁾ elucidated by using 4 hybrid cultures between f. sp. *tritici* and *agropyri* that several new resistant genes to *E. graminis* existed in wheat cultivars. These genes might not be identified without using hybrid cultures, probably because these genes had no function to *E. graminis* as in the case of *P. graminis*. In the past, these resistant genes probably had function to *E. graminis* f. sp. *tritici*, but derivation of races might have made them ineffective.

Tosa and Shishiyama²⁴⁾ concluded from the examination of the cellular defence reaction in barley cultivars that major genes for resistance to *E. graminis* f. sp. *hordei* are not involved in the resistance of barley cultivars to *E. graminis* f. sp. *tritici*. In the present paper, we found several new resistant genes different from some known genes to f. sp. *tritici* of *E. graminis* and they were summarized in Table 7. Powers and Sando²¹⁾ pointed out that the gene-for-gene hypothesis could be appreciable to host-parasite re-

Table 7. Gene symbols or resistant genes in wheat to culture t4 and to synthetic hybrids between formae speciales of *Erysiphe graminis*

Cultivar	Culture of <i>E. graminis</i>			
	t4	AT-N23	AT-C8	ST-N14
Little Club	—	<i>pm</i> -A1	<i>pm</i> -A4	<i>pm</i> -S1
Hard Federation	—	<i>Pm</i> -A2	—	—
Ramona 50	—	<i>Pm</i> -A3	—	—
Mayo 64	—	—	<i>Pm</i> -A5	<i>pm</i> -S2
Sinvalucho	—	—	<i>Pm</i> -A6	—
Axminster × Cc ⁸	<i>Pm</i> 1	—	<i>Pm</i> 1	—
Ulka × Cc ⁸	<i>Pm</i> 2	<i>Pm</i> 2	<i>Pm</i> 2	<i>Pm</i> 2
Asosan × Cc ⁸	<i>Pm</i> 3 a	<i>Pm</i> 3 a	<i>Pm</i> 3 a	<i>Pm</i> 3 a
Khapli × Cc ⁸	<i>Pm</i> 4 a	<i>Pm</i> 4 a	<i>Pm</i> 4 a	<i>Pm</i> 4 a

lationship of wheat-*E. graminis* system. The hybrid culture AT-C8 between f. sp. *agropyri* A1 and *tritici* t2 was not pathogenic to Axminster × Cc⁸ possessing *Pm*1 gene, which was resistant to t4 and susceptible to t2. This fact suggests that the resistant gene *Pm*1 is also functioning as avirulent gene originated from A1 of *E. graminis* f. sp. *agropyri*. Thus the race specific gene (or genes) for resistance could not be distinguished from specific genes against formae speciales from the genetical view point.

Thus, the number of genes for virulence accumulated in *E. graminis* to infect wheat may be reduced in the following order: *E. graminis* f. sp. *tritici*, hybrids, *E. graminis* f. sp. *agropyri* or f. sp. *secalis*. The difference between races of *E. graminis* f. sp. *tritici* and f. sp. *agropyri* or *secalis* seems to be indistinct, hence these three formae speciales are thought to be in the same category in a broad sense of race.

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和 文 摘 要

奥 尚・山下修一・土居養二・日浦運治：コムギ品種のイネ科植物うどんこ病菌 (*Erysiphe graminis* DC.) の分化型に対する抵抗性の遺伝学的解析

コムギ品種のイネ科植物うどんこ病菌 (*Erysiphe graminis* DC.) の分化型 (*formae speciales*) に対する抵抗性の遺伝様式を、f. sp. *tritici* (コムギ菌) 菌系 t2 × f. sp. *agropyri* (カモジグサ菌) 菌系 A1, t2 × f. sp. *secalis* (ライムギ菌) 菌系 S1 間の各雑種菌系および f. sp. *tritici* 菌系 t4 を用いて検討し、f. sp. *tritici*, f. sp. *agropyri* および f. sp. *secalis* のコムギ品種に対する寄生性の差異について考察した。雑種菌系のコムギ品種に対する病原性は、親の t2 に比べ若干低下し、特に t2 および t4 に罹病性の品種 Hard Federation, Little Club, Mayo 64, Sinvalucho などに対して非病原性となり注目された。これら品種の雑種菌系に対する抵抗性は、F₂ 試験により、既知遺伝子 *Pm1*, *Pm2*, *Pm3a* および *Pm4a* とは異なる遺伝子支配であった。雑種菌系を用いることによってのみ検出された抵抗性遺伝子は、f. sp. *agropyri* 菌系 A1 または f. sp. *secalis* 菌系 S1 由来の非病原性遺伝子に対応するもので、A1 または S1 は、t2 のコムギ品種に対する病原性遺伝子座に相当する座に非病原性遺伝子を持つと考えられた。Axminster × Cc⁸ は t2 に罹病性であったが、t4 および雑種菌系 AT-C8 に抵抗性で、両菌系を用いて既知遺伝子 *Pm1* が検出された。よって、*Pm1* に対する AT-C8 の f. sp. *agropyri* 菌系 A1 由来の非病原性遺伝子は f. sp. *tritici* 菌系 t4 のそれと同一であり、f. sp. *tritici* のレースに対する抵抗性遺伝子が、他の分化型に対する抵抗性にも関与することが判明した。以上の知見により、コムギ品種に対する各菌系の病原性遺伝子数は多数持つものから t2, t4, 雑種, A1 または S1 の順と推定され、*E. graminis* DC. の分化型のコムギ品種に対する寄生性の差異は、各々のコムギ品種に対する病原性遺伝子の集積度の差によるものと推定された。